

-Sund 1/20/2006 + 1/20/2006

Fig 1a

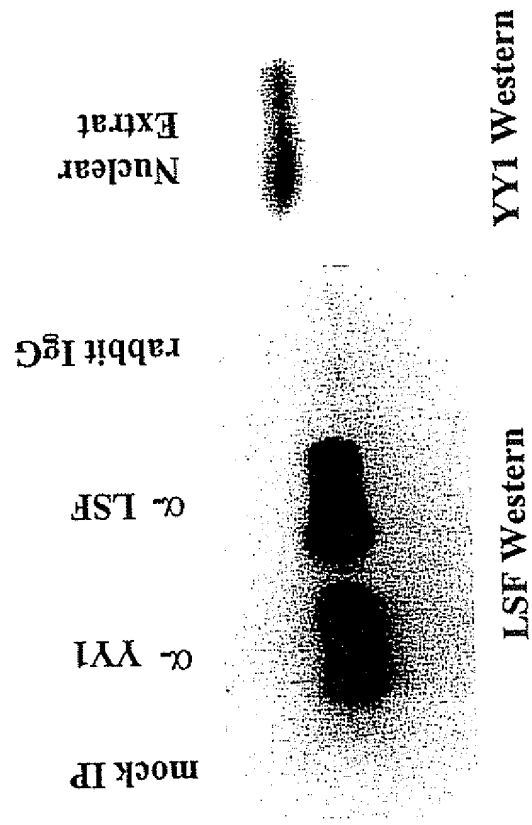


Fig 1b

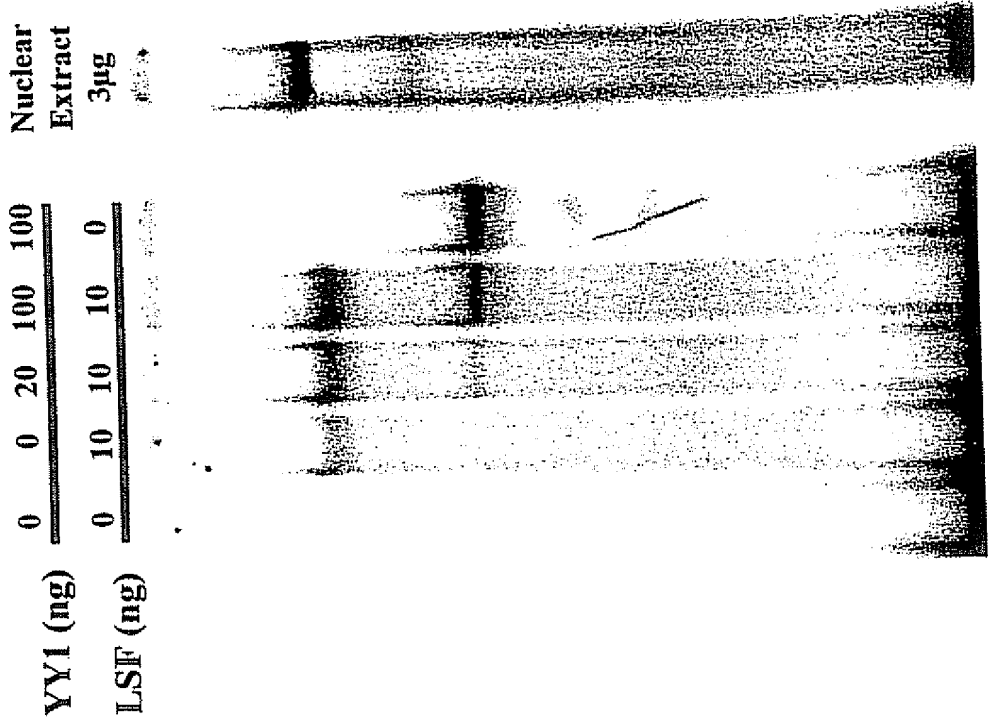


Fig. 1c

LSF (ng)	10			20	40
YY1 (30 ng)	-	+	+	-	-
α -YY1	-	-	+	-	-
α -LSF	-	-	-	+	-

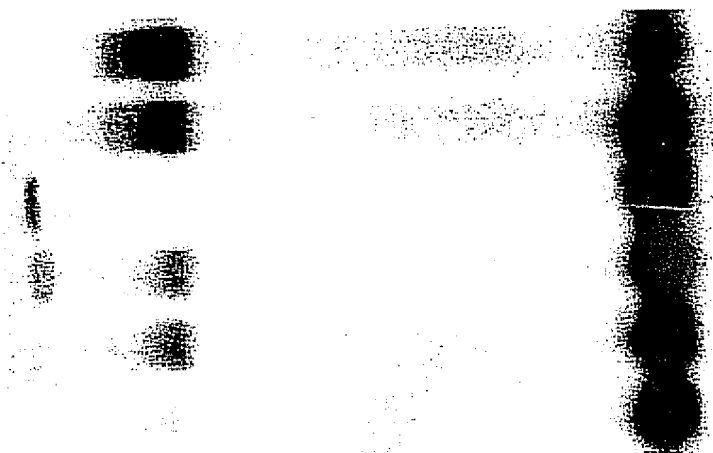


Fig 2a

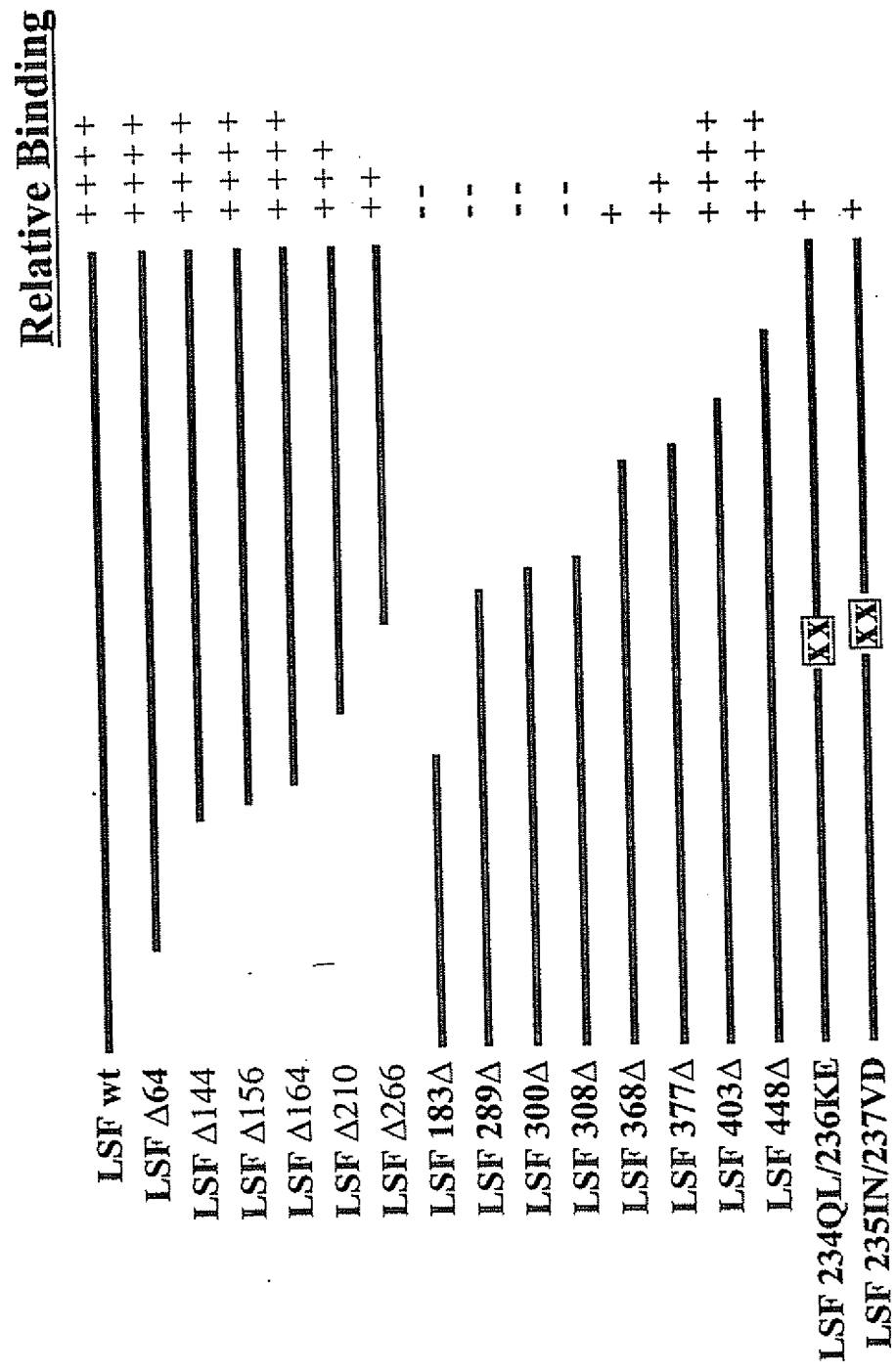


Fig 2b

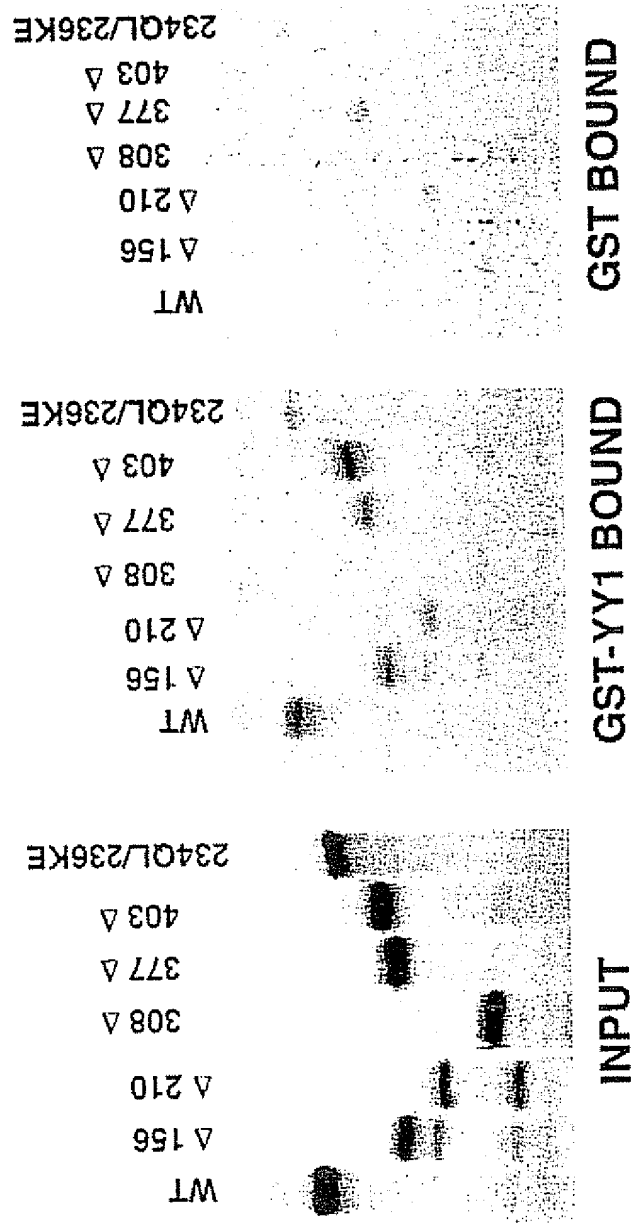


Fig 2c

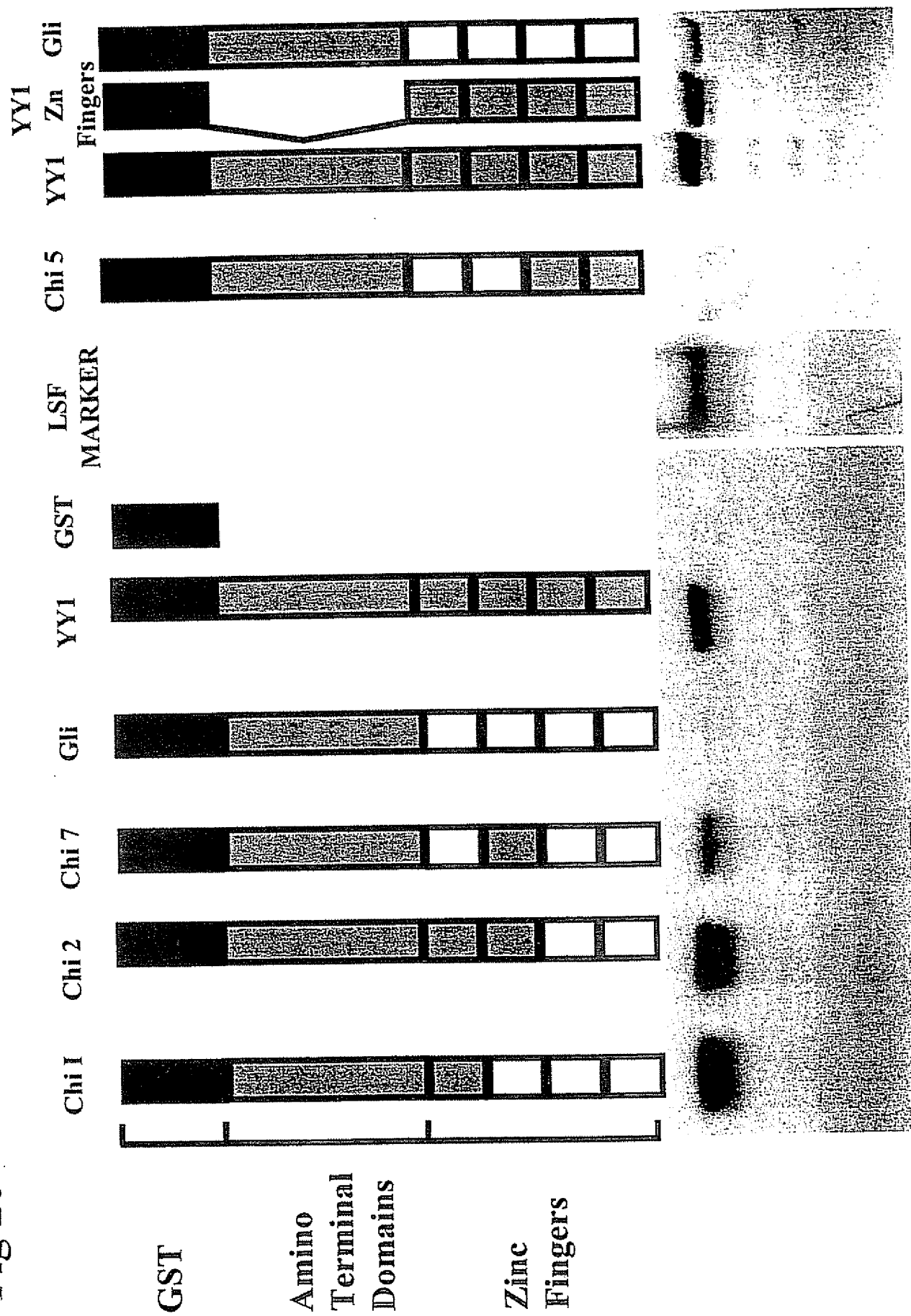


Fig 3

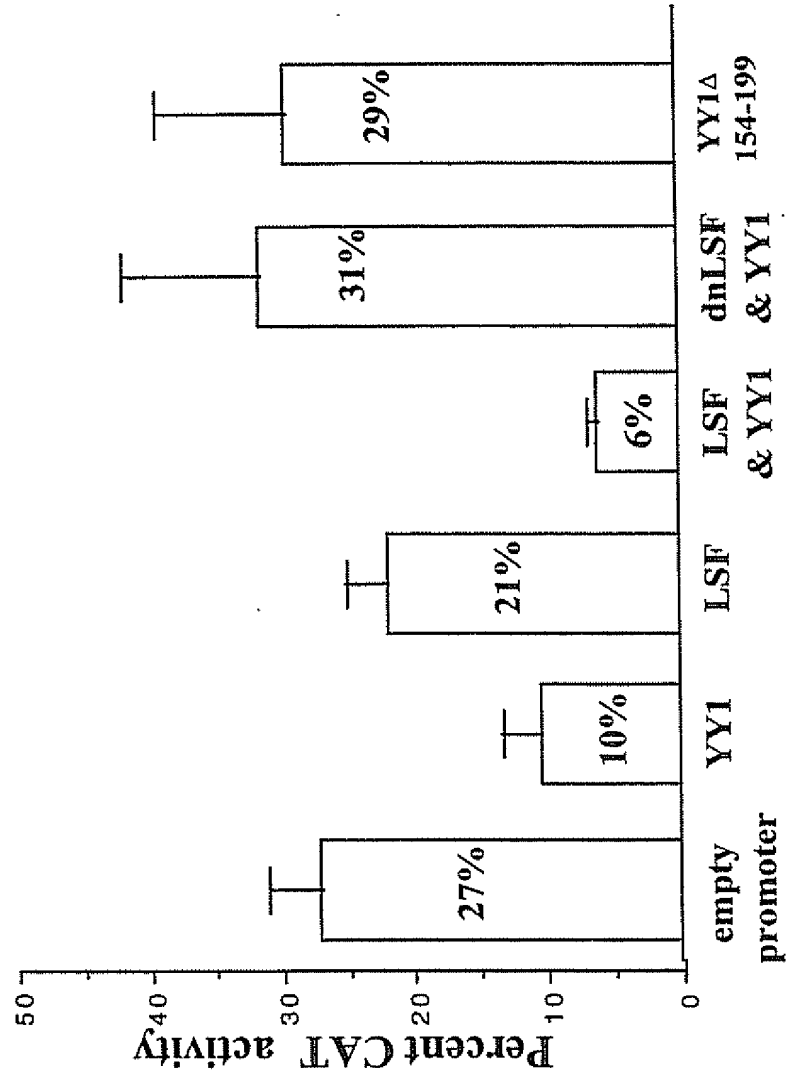


Fig 4a

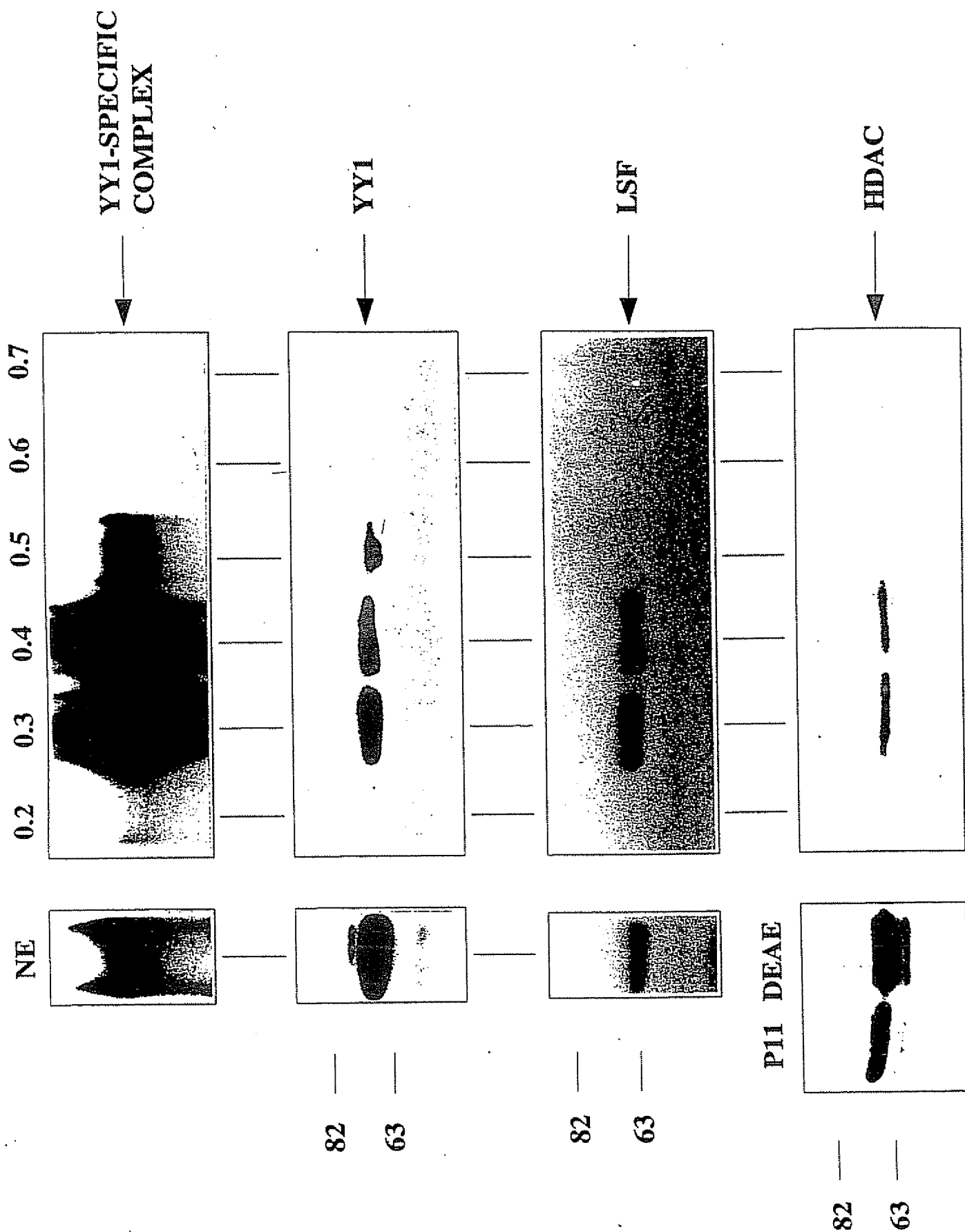


Fig 4b

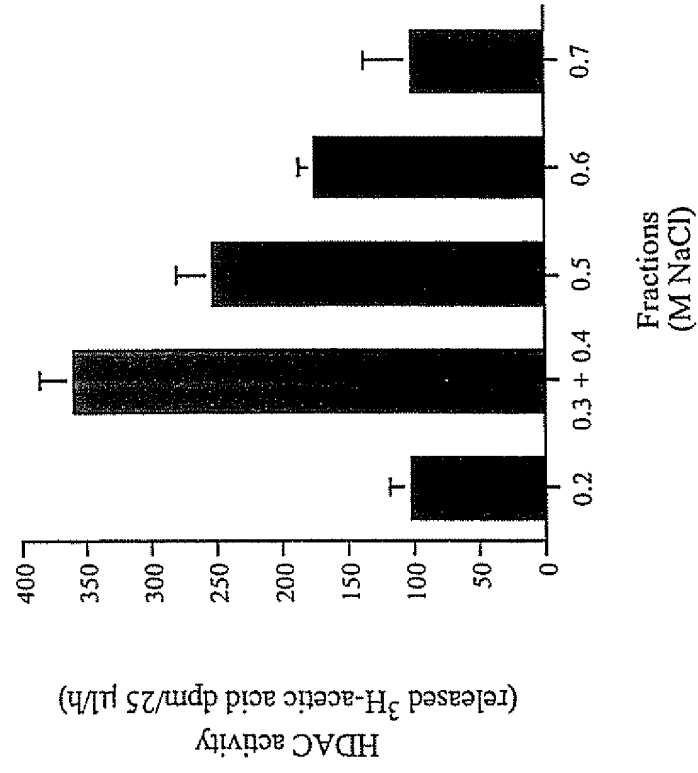


Fig 5

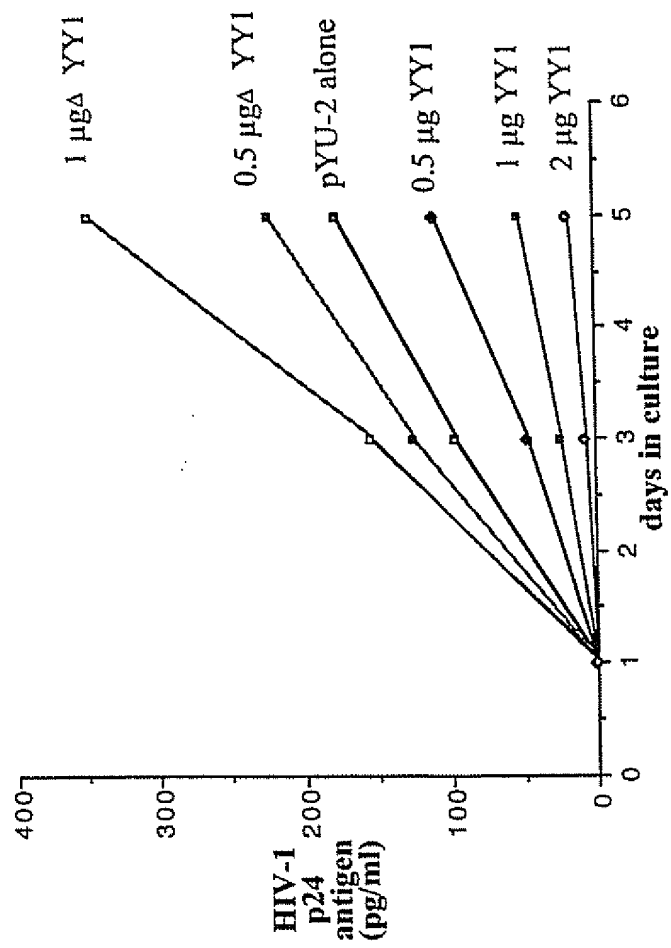
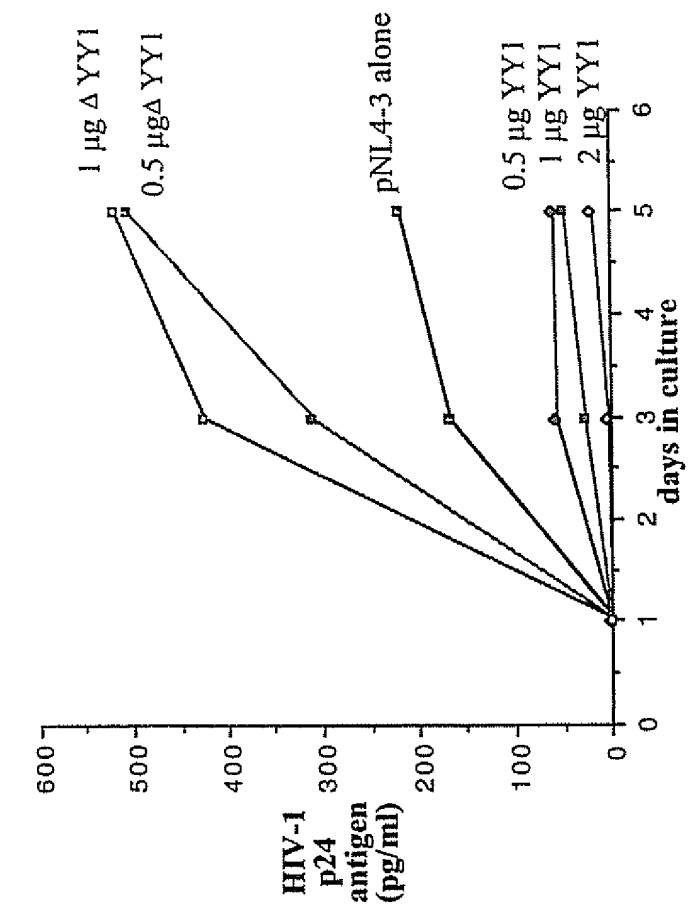
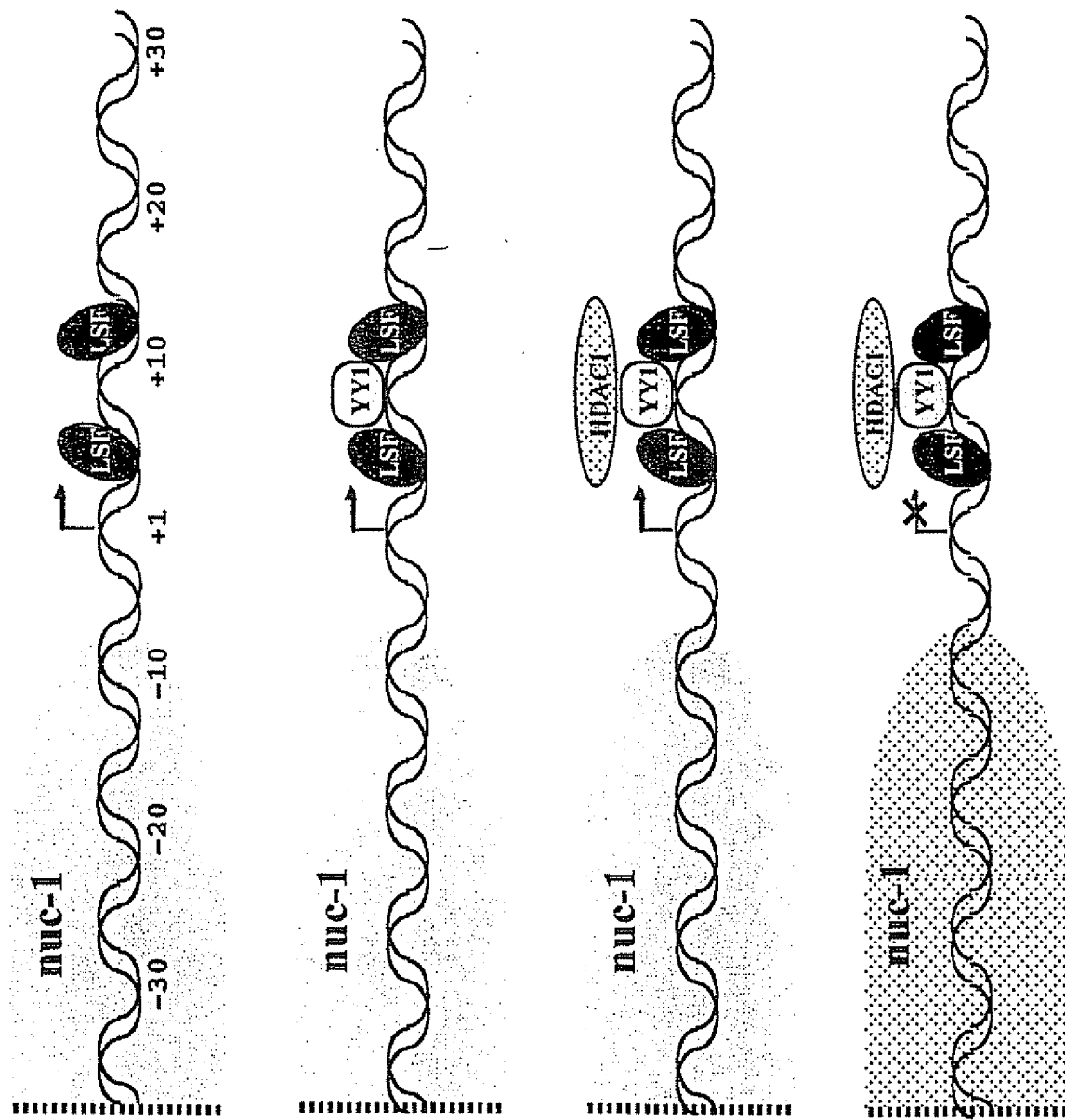


Fig 6



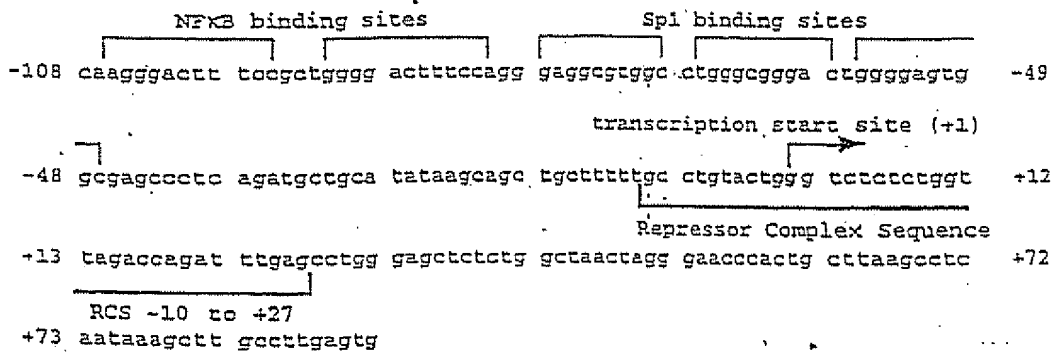


FIG. 7

CGCCGAGACG AGCAGCGGCC GAGCGAGCGC GGGCGCGGGC GCACCGAGGC GAGGGAGGGC	60
GGGAAGCCCC GCGCGCCCGC CCGCGCCCGC CCCTTCCCCC GCGCGCCCGC CCCTCTCCCC	120
CCGCCCCGTC GCGCCCTTCC TCCTCTCTGCC TTCCTTCCCC ACGGCGCGGC GCCTCTCGC	180
CCGCCCCGCC GCAGCCGAGG AGCCGAGGCC GCGCGCGCGC TGGCGGCGGA GCCCTCAGCC	240
ATG GCC TCG GGC GAC ACC CTC TAC ATC GCC ACG GAC GGC TCG GAG ATG	288
Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met	
1 5 10 15	
CCG GCC GAG ATC GTG GAG CTG CAC GAG ATC GAG GTG GAG ACC ATC CCG	336
Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro	
20 25 30	
GTG GAG ACC ATC GAG ACC ACA GTG GTG GGC GAG GAG GAG GAG GAG GAC	384
Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Glu Asp	
35 40 45	
GAC GAC GAC GAG GAC GGC GGC GGT GGC GAC CAC GGC GGC GGC GGC GGC	432
Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly	
50 55 60	
CAC GGC CAC GCC GGC CAC CAC CAC CAC CAC CAT CAC CAC CAC CAC CAC	480
His Gly His Ala Gly His His His His His His His His His His His	
65 70 75 80	
CCG CCC ATG ATC GCT CTG CAG CCG CTG GTC ACC GAC GAC CCG ACC CAG	528
Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln	
85 90 95	
GTG CAC CAC CAC CAG GAG GTG ATC CTG GTG CAG ACG CGC GAG GAG GTG	576
Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val	
100 105 110	
GTG GGC GGC GAC GAC TCG GAC GGC CTG CGC GCC GAG GAC GGC TTC GAG	624
Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu	
115 120 125	
GAT CAG ATT CTC ATC CCG GTG CCC GCG CCG GCC GGC GGC GAC GAC GAC	672
Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp	
130 135 140	
TAC ATT GAA CAA ACG CTG GTC ACC GTG GCG GCG GCC GGC AAG AGC GGC	720
Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly	
145 150 155 160	
GGC GGC GGC TCG TCG TCG TCG GGA GGC GGC CGC GTC AAG AAG GGC GGC	768
Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly	
165 170 175	
GGC AAG AAG AGC GGC AAG AAG AGT TAC CTC AGC GGC GGC GCC GGC GCG	816
Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala	
180 185 190	
GCG GGC GGC CGC GGC GCC GAC CCG GGC AAC AAG AAG TGG GAG CAG AAG	864
Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys	
195 200 205	
CAG GTG CAG ATC AAG ACC CTG GAG GGC GAG TTC TCG GTC ACC ATG TGG	912
Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp	
210 215 220	
TCC TCA GAT GAA AAA AAA GAT ATT GAC CAT GAG ACA GTG GTT GAA GAA	960
Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu	
225 230 235 240	
CAG ATC ATT GGA GAG AAC TCA CCT CCT GAT TAT TCA GAA TAT ATG ACA	1008
Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr	
245 250 255	

GGA AAG AAA CTT CCT CCT GGA GGA ATA CCT GGC ATT GAC CTC TCA GAT	1056
Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp	
260 265 270	
CCC AAA CAA CTG GCA GAA TTT GCT AGA ATG AAG CCA AGA AAA ATT AAA	1104
Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys	
275 280 285	
GAA GAT GAT GCT CCA AGA ACA ATA GCT TGC CCT CAT AAA GGC TGC ACA	1152
Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr	
290 295 300	
AAG ATG TTC AGG GAT AAC TCG GCC ATG AGA AAA CAT CTG CAC ACC CAC	1200
Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His	
305 310 315 320	
GGT CCC AGA GTC CAC GTC TGT GCA GAA TGT GGC AAA GCT TTT GTT GAG	1248
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu	
325 330 335	
AGT TCA AAA CTA AAA CGA CAC CAA CTG GTT CAT ACT GGA GAG AAG CCC	1296
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro	
340 345 350	
TTT CAG TGC ACG TTC GAA GGC TGT GGG AAA CGC TTT TCA CTG GAC TTC	1344
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe	
355 360 365	
AAT TTG CGC ACA CAT GTG CGA ATC CAT ACC GGA GAC AGG CCC TAT GTG	1392
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val	
370 375 380	
TGC CCC TTC GAT GGT TGT AAT AAG AAG TTT GCT CAG TCA ACT AAC CTG	1440
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu	
385 390 395 400	
AAA TCT CAC ATC TTA ACA CAT GCT AAG GCC AAA AAC AAC CAG TGAAAAGAA	1491
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln	
405 410	
GAGAGAGAC CCTTCTCGAC CACGGGAGGC ATCTTCCAGA AGTGTGATTG GGAATAAATA	1551
TGCCTCTCCT TTGTATATTA TTTCTAGGAA GAATTTTAAA AATGAATCCT ACACACCTAA	1611
GGGACATGTT TTGATAAAGT AGTAAAAATT AAAAAAAAAA AACTTTACTA AGATGACATT	1671
GCTAAGATGC TCTATCTTGC TCTGTAACTCT CGTTTCAAA ACACAGTGTT TTTGTAAAGT	1731
GTGGTCCCAA CAGGAGGACA ATTCATGAAC TTCGCATCAA AAGACAATTC TTTATACAAC	1791
AGTGCTAAAA ATGGGACTTC TTTTCACATT CTTATAAATA TGAAGCTCAC CTGTTGCTTA	1851
CAATTTTTTT AATTTTGTAT TTTCCAAGTG TGCATATTGT ACACTTTTTT GGGGATATGC	1911
TTAGTAATGC TACGTGTGAT TTTTCTGGAG GTTGATAACT TTGCTTGCAG TAGATTTTCT	1971
TTAAAAGAAT GGGCAGTTAC ATGCATACTT CAAAAGTATT TTCCTGTAAA AAAAAAAAAA	2031
GTTATATAGG TTTTGTTCG TATCTTAATT TTGGTTGTAT TCTTTGATGT TAACACATTT	2091
TGTATAATTG TATCGTATAG CTGTATTGAA TCATGTAGTA TCAAATATTA GATGTGATTT	2151
AATAGTGTTA ATCAATTAA ACCCATTTTA GTCACTTTTT TTTTCCAAA AATACTGCC	2211
AGATGCTGAT GTTCAGTGTA ATTTCTTTGC CTGTTCAAGT ACAGAAAGTG GTGCTCAGTT	2271
GTAGAATGTA TTGTACCTTT TAACACCTGA TGTGTACATC CCATGTAACA GAAAGGGCAA	2331
CAATAAATA GCAATCCTAA AG	2353

FIG 8
(contd)

GAGGACGCCA	TCATTGGTTG	CGCCTGGGGC	GGCCGACCGT	GGAAGGGCCT	GGCGAGTCTA	60
GGTTTTACGC	CTGTGCTGGA	CTTTCTCCTT	CCATGTTTCC	AGGCCGTGGG	GGGCTACAGA	120
GGCCGAGAAG	TCGGCTCAGC	GGAAACCTGG	ATTTGGTTCT	AAGCCGTGGG	GTTGAGAAGG	180
GGTGACCGGA	AGTGATCGTG	GGACTGACCG	GAAGCGAGGC	CTGGAGGGGA	AAGAGAGAGC	240
GAGACCTGGG	AGGGAGGGGG	CCTCCAGCAG	AAAGGGGCGG	GGGAAAAGGT	GCAAAAGCAG	300
CGTGGGAGCG	CCGGCTGGGC	TTCCTGCGGC	TGCTGCTGGT	CTGACTGGGA	AGCAGCAAGC	360
CACCACTACG	AACCTCTCAAG	AGGAGTGGGA	GTGCGGGAGT	CCAGAGCTGC	CTCTGGGAAG	420
TCTGCASTAG	TTGAGCAAG	GGGTCTCTAC	GTTCTTGAGA	GCTGGGCAGG	GGGGATTTTG	480
GAACCTGGGG	CAGCCAAGAA	CGAGCAGCCA	AGGGTACGGG	AGATTAGTTG	TGCACAGAGC	540
AGTGCTGGTC	GGGCTTGGGG	GTGGCTGGTG	GGCACTGCGT	GGGAAACCTT	GGTTTGTAGT	600
TTTCTTGGTT	TGCGTTACTC	CTGTTGGGTA	GAATTACCCT	CCGCGCCTTT	GTACAAGACA	660
CGGTGTCTCC	TGGGGCAAGG	AAGGAGCCAG	G	ATG GCC TGG GCT CTG	AAG CTG	712
			Met Ala Trp Ala Leu Lys Leu			
			1	5		
CCT CTG GCC GAC GAA GTG ATT GAA TCC GGG TTG GTG CAG GAC TTT GAT						760
Pro Leu Ala Asp Glu Val Ile Glu Ser Gly Leu Val Gln Asp Phe Asp						
10	15	20				
GCT AGC CTG TCC GGG ATC GGC CAG GAA CTG GGT GCT GGT GCC TAT AGC						808
Ala Ser Leu Ser Gly Ile Gly Gln Glu Leu Gly Ala Gly Ala Tyr Ser						
25	30	35				
ATG AGT GAT GTC CTT GCA TTG CCC ATT TTT AAG CAA GAA GAG TCG AGT						856
Met Ser Asp Val Leu Ala Leu Pro Ile Phe Lys Gln Glu Glu Ser Ser						
40	45	50	55			
TTG CCT CCT GAT AAT GAG AAT AAA ATC CTG CCT TTT CAA TAT GTG CTT						904
Leu Pro Pro Asp Asn Glu Asn Lys Ile Leu Pro Phe Gln Tyr Val Leu						
60	65	70				
TGT GCT GCT ACC TCT CCA GCA GTG AAA CTC CAT GAT GAA ACC CTA ACC						952
Cys Ala Ala Thr Ser Pro Ala Val Lys Leu His Asp Glu Thr Leu Thr						
75	80	85				
TAT CTC AAT CAA GGA CAG TCT TAT GAA ATT CGA ATG CTA GAC AAT AGG						1000
Tyr Leu Asn Gln Gly Gln Ser Tyr Glu Ile Arg Met Leu Asp Asn Arg						
90	95	100				
AAA CTT GGA GAA CTT CCA GAA ATT AAT GGC AAA TTG GTG AAG ACT ATA						1048
Lys Leu Gly Glu Leu Pro Glu Ile Asn Gly Lys Leu Val Lys Ser Ile						
105	110	115				
TTC CGT GTG GTG TTC CAT GAC AGA AGG CTT CAG TAC ACT GAG CAT CAG						1096
Phe Arg Val Val Phe His Asp Arg Arg Leu Gln Tyr Thr Glu His Gln						
120	125	130	135			
CAG CTA GAG GGC TGG AGG TGG AAC CGA CCT GGA GAC AGA ATT CTT GAC						1144
Gln Leu Glu Gly Trp Arg Trp Asn Arg Pro Gly Asp Arg Ile Leu Asp						
140	145	150				
ATA GAT ATC CCG ATG TCT GTG GGT ATA ATC GAT CCT AGG GCT AAT CCA						1192
Ile Asp Ile Pro Met Ser Val Gly Ile Ile Asp Pro Arg Ala Asn Pro						
155	160	165				
ACT CAA CTA AAT ACA GTG GAG TTC CTG TGG GAC CCT GCA AAG AGG ACA						1240
Thr Gln Leu Asn Thr Val Glu Phe Leu Trp Asp Pro Ala Lys Arg Thr						
170	175	180				
TCT GTG TTT ATT CAG GTG CAC TGT ATT AGC ACA GAG TTC ACT ATG AGG						1288
Ser Val Phe Ile Gln Val His Cys Ile Ser Thr Glu Phe Thr Met Arg						
185	190	195				
AAA CAT GCC GGA GAA AAG GGG GTG CCA TTC CGA GTA CAA ATA GAT ACC						1336
Lys His Gly Gly Glu Lys Gly Val Pro Phe Arg Val Gln Ile Asp Thr						
200	205	210	215			

FIGURE 10A

(SEQ ID NO: 6)

Human Histone Deacetylase 1 - Protein Sequence

[NCBI Gen Bank Accession No. NP 004955]

ORIGIN

```
1 maqtqgtrrk vcyydgdv nyyygqghpm kphirmthn llnyglyrk meiyprhkan
61 aeemtkyhsd dyikflrsir pdnmseyskq mqrfnvgedc pvfdglfefe qlstggsvas
121 avklnkqgtd iawnwagglh hakkseasgf cyvndivlai lellkyhqr v lyididihhg
181 dgveeafytt drvmtvsfhk ygeyfpgtgd lrdigagkgk yyavnyplrd giddesyeai
241 fkpvmaskvme mfqpsavvlq cgsdslsgdr lgcfnltikg hakcvefvks fnlpmlmlgg
301 ggytirnvar crtvetaval dteipnelpy ndyfeyfgpd fklhispsnm tnqntneyle
361 kikqrlfenl rmlphapgvq mqaipedaip eesgdededd pdkrisicss dkriaceeef
421 sdseeegegg rkssnfkka krvtedeke kdpeekkev t eeektkeekp eakgvkeevk
481 la
```


FIGURE 10B
(SEQ ID NO: 7)
Human Histone Deacetylase 1 mRNA Sequence
[NCBI Gen Bank Accession No. NP 004964]

ORIGIN

```
1 gagcggagcc gcgggcgga gggcgacgg accgactgac gtagggacg ggagggcagc
61 aagatggcgc agacgcaggg caccggagg aaagtctgtt actactacga cggggatgtt
121 ggaaattact attatggaca aggccacca atgaagcctc accgaatccg catgactcat
181 aatttgctgc tcaactatgg tctctaccga aaaatggaaa tctatcgccc tcacaaagcc
241 aatgctgagg agatgaccaa gtaccacagc gatgactaca ttaaattctt ggcctccatc
301 cgtccagata acatgtcgga gtacagcaag cagatgcaga gattcaacgt tggtagggac
361 tgtccagtat tccatggcct gtttgagttc tgcagttgt ctactgggtg ttctgtggca
421 agtgctgtga aacttaataa gcagcagacg gacatcgctg tgaattgggc tgggggcctg
481 caccatgcaa agaagtccga ggcactctggc ttctgttacg tcaatgatat cgtcttggcc
541 atcctggaac tgctaaagta tcaccagagg gtgctgtaca ttgacattga tattcaccat
601 ggtgacggcg tggaagaggc cttctacacc acggaccggg tcatgactgt gtcctttcat
661 aagtatggag agtacttccc aggaactggg gacctacggg atatcggggc tggcaaaggc
721 aagtattatg ctgttaacta cccgctccga gacgggattg atgacgagtc ctatgaggcc
781 attttcaagc cggtcattgtc caaagtaatg gagatgttcc agcctagtgc ggtggtctta
841 cagtgtggct cagactccct atctggggat cggttagggt gcttcaatct aactatcaaa
901 ggacacgcca agtgtgtgga atttgtcaag agctttaacc tgcctatgct gatgctggga
961 ggcgggtggtt acaccattcg taacgttgcc cgggtgcagga catatgagac agctgtggcc
1021 ctggatacgg agatccctaa tgagcttoca tacaatgact actttgaata ctttggacca
1081 gatttcaagc tccacatcag tccttccaat atgactaacc agaacacgaa tgagtacctg
1141 gagaagatca aacagcgact gtttgagaac cttagaatgc tgccgcacgc acctggggtc
1201 caaatgcagg cgattcctga ggacgccatc cctgaggaga gtggcgatga ggacgaagac
1261 gacctgaca agcgcactctc gatctgctcc tctgacaaac gaattgcctg tgaggaagag
1321 ttctccgatt ctgaagagga gggagagggg ggccgcaaga actcttccaa cttcaaaaaa
1381 gccaaagagag tcaaaacaga ggatgaaaaa gagaaagacc cagaggagaa gaaagaagtc
1441 accgaagagg agaaaaccaa ggaggagaag ccagaagcca aaggggtcaa ggaggaggtc
```

1501 aagttggcct gaatggacct ctccagctct ggcttcctgc tgagtcctc acgtttcttc
1561 cccaaccct cagattttat atttctatt tctctgtgta tttatataaa aattttattaa
1621 atataaatat cccagggac agaaaccaag gccccgagct cagggcagct gtgctgggtg
1681 agctcttcca ggagccacct tgccaccat tcttcccgtt cttactttg aaccataaag
1741 ggtgccaggt ctgggtgaaa gggatacttt tatgcaacca taagacaaac tcctgaaatg
1801 ccaagtgcct gcttagtagc tttggaaagg tgcccttatt gaacattcta gaaggggtgg
1861 ctgggtcttc aaggatctcc tgtttttttc aggctcctaa agtaacatca gccattttta
1921 gattggttct gttttcgtac ctccactg gcctcaagtg agccaagaaa cactgcctgc
1981 cctctgtctg tcttctccta attctgcagg tggaggttgc tagtctagtt tcctttttga
2041 gatactatct tcatttttgt gagcctcttt gtaataaaat ggtacatttc t

FIGURE 10B Continued